

## BLAST 2 SEQUENCES

This functionality is now available in the main [BLAST](#) pages and this link will be removed in the near future. [Step-by-step instructions](#) for use are available.

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

[Reference](#): Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in [BLASTN](#) program only:

Reward for a match:  Penalty for a mismatch:

☐ Use [Mega BLAST](#) Strand option  View option

Masking character option  Masking color option

☐ Show CDS translation

Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒

Sequence 1

Enter accession, GI or sequence in FASTA format from:  to:

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttgcg ttttggcact caaaagtatg tccagaaaat
cccagcgctt tttctgagta gtatcttggt ttagcttatc ctttaagagac
tccttcgggt cctggattac tttctctgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from:  to:

```
H21976
```

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



# Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☒ View option   
Masking character option  Masking color option   
☐ Show CDS translation

---

Sequence 1: lcl1

Length = 379

Sequence 2: [gil890671|yl138c11.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:160532 5' similar to SP:CP4B\\_RABIT P15128 CYTOCHROME P450 IVB1 ;, mRNA sequence.](#)

Length = 332

No significant similarity was found

CPU time:        0.04 user secs.            0.04 sys. secs            0.08 total secs.

## BLAST 2 SEQUENCES

This functionality is now available in the main [BLAST](#) pages and this link will be removed in the near future. [Step-by-step instructions](#) for use are available.

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)  
[Reference](#): Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in [BLASTN](#) program only:

Reward for a match:  Penalty for a mismatch:

☐ Use [Mega BLAST](#) Strand option  View option   
Masking character option  Masking color option   
☐ Show CDS translation

Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒

Sequence 1

Enter accession, GI or sequence in FASTA format from:  to:

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttcgc ttttggcact caaaagtatg tccagaaaat
cccagcgctt tttctgagta gtatcttggt ttagcttatc ctttaagagac
tccttcgggt cctggattac tttctctgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from:  to:

```
H21977
```

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



# Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☒ View option   
Masking character option  Masking color option   
☐ Show CDS translation

---

Sequence 1: lcl1

Length = 379

Sequence 2: [gil890672|yl138c11.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:160532 3', mRNA sequence.](#)

Length = 444

No significant similarity was found

CPU time:      0.03 user secs.      0.01 sys. secs      0.04 total secs.

## BLAST 2 SEQUENCES

This functionality is now available in the main [BLAST](#) pages and this link will be removed in the near future. [Step-by-step instructions](#) for use are available.

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

[Reference](#): Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in [BLASTN](#) program only:

Reward for a match:  Penalty for a mismatch:

☐ Use [Mega BLAST](#) Strand option  View option

Masking character option  Masking color option

☐ Show CDS translation

Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒

Sequence 1

Enter accession, GI or sequence in FASTA format from:  to:

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttcgc ttttggcact caaaagtatg tccagaaaat
cccagcgctt tttctgagta gtatcttggt ttagcttatc ctttaagagac
tccttcgggt cctggattac tttctctgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from:  to:

```
H25577
```

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



# Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match:  Mismatch:  gap open:  gap extension:

x\_dropoff:  expect:  wordsize:  Filter ☒ View option

Masking character option  Masking color option

☐ Show CDS translation

---

Sequence 1: lcl1

Length = 379

Sequence 2: [gil894700|yl148g04.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:161526 3', mRNA sequence.](#)

Length = 421

No significant similarity was found

CPU time:      0.04 user secs.      0.03 sys. secs      0.07 total secs.

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

## BLAST 2 SEQUENCES

This functionality is now available in the main [BLAST](#) pages and this link will be removed in the near future. [Step-by-step instructions](#) for use are available.

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

[Reference](#): Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in [BLASTN](#) program only:

Reward for a match:  Penalty for a mismatch:

☐ Use [Mega BLAST](#) Strand option  View option

Masking character option  Masking color option

☐ Show CDS translation

Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒

Sequence 1

Enter accession, GI or sequence in FASTA format from:  to:

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttgcg ttttggcact caaaagtatg tccagaaaat
cccagcgctt tttctgagta gtatcttggt ttagcttatc cttaaagagac
tccttcgggt cctggattac tttctctgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from:  to:

```
H25624
```

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



# Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☒ View option   
Masking character option  Masking color option   
☐ Show CDS translation

---

Sequence 1: lcl1

Length = 379

Sequence 2: [gil894747|yl148g04.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:161526 5' similar to gb:J02871 CYTOCHROME P450 IVB1 \(HUMAN\);contains Alu repetitive element;. mRNA sequence.](#)

Length = 432

No significant similarity was found

CPU time:        0.04 user secs.            0.03 sys. secs            0.07 total secs.



## BLAST 2 SEQUENCES

This functionality is now available in the main [BLAST](#) pages and this link will be removed in the near future. [Step-by-step instructions](#) for use are available.

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)  
[Reference](#): Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in [BLASTN](#) program only:

Reward for a match:  Penalty for a mismatch:

☐ Use [Mega BLAST](#) Strand option  View option   
Masking character option  Masking color option   
☐ Show CDS translation

Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter ☒

Sequence 1

Enter accession, GI or sequence in FASTA format from:  to:

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttcgc ttttggcact caaaagtatg tccagaaaat
cccagcgctt tttctgagta gtatcttggt ttagcttatc ctttaagagac
tccttcgggt cctggattac tttctctgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from:  to:

```
AA003705
```

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



# Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match:  Mismatch:  gap open:  gap extension:

x\_dropoff:  expect:  wordsize:  Filter ☒ View option

Masking character option  Masking color option

☐ Show CDS translation

---

Sequence 1: lcl1

Length = 379

Sequence 2: [gil1447205img61a02.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:437450 5', mRNA sequence.](#)

Length = 331

No significant similarity was found

CPU time:      0.02 user secs.      0.03 sys. secs      0.05 total secs.